

RAW SEQUENCE LISTING
PATENT APPLICATION US/07/938,154DATE: 03/08/94
TIME: 12:25:06

INPUT SET: S7462.raw

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Harpold, Michael M.
Ellis, Stephen B.
Brust, Paul
Akong, Michael
Velicelebi, Gonul

(ii) TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pretty Schroeder Brueggemann & Clark
(B) STREET: 444 South Flower Street, Suite 2000
(C) CITY: Los Angeles
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 90071

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/938,154
(B) FILING DATE: 30-NOV-1992
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/US91/02311
(B) FILING DATE: 03-APR-1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/504,455
(B) FILING DATE: 03-APR-1990

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reiter, Stephen E.
(B) REGISTRATION NUMBER: 31,192
(C) REFERENCE/DOCKET NUMBER: P41 9380

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-546-4737
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52

53 (2) INFORMATION FOR SEQ ID NO:1:

54

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 195 base pairs

57 (B) TYPE: nucleic acid

58 (C) STRANDEDNESS: both

59 (D) TOPOLOGY: both

60

61 (ii) MOLECULE TYPE: cDNA

62

63

64

65

66

67 (ix) FEATURE:

68 (A) NAME/KEY: misc_feature

69 (B) LOCATION: 1..195

70 (D) OTHER INFORMATION: /note= "Human neuronal NACHR
71 alpha-2 cDNA shown as top sequence of Fig 7A."

72

73

74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

75

76 GCTAAACAGG AGTGGAGCGA CTACAACTG CGCTGGAACC CCGCTGATTT TGGCAACATC 60

77

78 ACATCTCTCA GGGTCCCTTC TGAGATGATC TGGATCCCCG ACATTGTTCT CTACAACAAA 120

79

80 AATGGGGAGT TTGCAGTGAC CCACATGACC AAGGCCACCC TCTTCTCCAC GGGCACTGTG 180

81

82 CACTGGGTGC CCCCC 195

83

84 (2) INFORMATION FOR SEQ ID NO:2:

85

86 (i) SEQUENCE CHARACTERISTICS:

87 (A) LENGTH: 209 base pairs

88 (B) TYPE: nucleic acid

89 (C) STRANDEDNESS: both

90 (D) TOPOLOGY: both

91

92 (ii) MOLECULE TYPE: cDNA

93

94

95 (ix) FEATURE:

96 (A) NAME/KEY: misc_feature

97 (B) LOCATION: 1..209

98 (D) OTHER INFORMATION: /note= "Rat neuronal NACHR alpha-2
99 cDNA shown as the bottom nucleotide sequence in
100 Figure 7A."

101

102

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103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
104
105 CCAATGTCTG GCTAAAGCAG GAATGGAATG ACTACAAGCT GCGCTGGGAC CCGGCTGAGT 60
106
107 TTGGCAATGT CACCTCCCTG CGCGTCCCTT CAGAGATGAT CTGGATCCCA GACATTGTCC 120
108
109 TCTACAACAA TGCAGATGGG GAGTTTGCGG TGACCCACAT GACCAAGGCT CACCTCTTCT 180
110
111 TCACGGGCAC TGTGCACTGG GTGCCCCCA 209
112
113 (2) INFORMATION FOR SEQ ID NO:3:
114
115 (i) SEQUENCE CHARACTERISTICS:
116 (A) LENGTH: 202 base pairs
117 (B) TYPE: nucleic acid
118 (C) STRANDEDNESS: both
119 (D) TOPOLOGY: both
120
121 (ii) MOLECULE TYPE: cDNA
122
123
124 (ix) FEATURE:
125 (A) NAME/KEY: misc_feature
126 (B) LOCATION: 1..202
127 (D) OTHER INFORMATION: /note= "Human neuronal NACHR
128 alpha-2 cDNA shown as top sequence in Fig 7B."
129
130
131
132
133
134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
135
136 CCCCTTCGAC CAGCAGAACT GCAAGATGAA GTTTGGCTCC TGGACTTATG ACAAGGCCAA 60
137
138 GATCGACCTG GAGCAGATGG AGCAGACTGT GGACCTGAAG GACTACTGGG AGAGCGGCCGA 120
139
140 GTGGGCCATC GTCAATGCCA CGGGCACCTA CAACAGCAAG AAGTACGACT GCTGCGCCGA 180
141
142 GATCTACCCC GACGTCACCT AG 202
143
144 (2) INFORMATION FOR SEQ ID NO:4:
145
146 (i) SEQUENCE CHARACTERISTICS:
147 (A) LENGTH: 250 base pairs
148 (B) TYPE: nucleic acid
149 (C) STRANDEDNESS: both
150 (D) TOPOLOGY: both
151
152 (ii) MOLECULE TYPE: cDNA
153

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154 (ix) FEATURE:
155 (A) NAME/KEY: misc_feature
156 (B) LOCATION: 1..250
157 (D) OTHER INFORMATION: /note= "Rat neuronal NACHR alpha-2
158 cDNA shown as bottom sequence in Fig 7B."
159
160
161 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
162
163 CCCCTTCGAC CAGCAGAACT GCAAGATGAA GTTTGGCTCC TGGACATATG ACAAGGCCAA 60
164
165 GATCGATCTG GAGCAGATGG AGAGGACAGT GGACCTGAAG GACTACTGGG AGAGTGGCGA 120
166
167 GTGGGCCATT ATCAATGCCA CCGGAACCTA TAACAGTAAG AAGTACGACT GCTGCGCGGA 180
168
169 GATCTACCCC GATGTCACCT ACTACTTTGT GATCCGGCGG CTGCCGCTGT TCTATACCAT 240
170
171 CAACCTCATC 250
172
173 (2) INFORMATION FOR SEQ ID NO:5:
174
175 (i) SEQUENCE CHARACTERISTICS:
176 (A) LENGTH: 278 base pairs
177 (B) TYPE: nucleic acid
178 (C) STRANDEDNESS: both
179 (D) TOPOLOGY: both
180
181 (ii) MOLECULE TYPE: cDNA
182
183 (ix) FEATURE:
184 (A) NAME/KEY: misc_feature
185 (B) LOCATION: 1..278
186 (D) OTHER INFORMATION: /note= "Human neuronal NACHR
187 alpha-3 cDNA shown as top sequence in Fig 8A."
188
189
190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
191
192 CTGGCAGCAG AGGCTGAGCA CCGTCTATTT GAGCGGCTGT TTGAAGATTA CAATGAGATC 60
193
194 ATCCGGCCTG TAGCCAACGT GTCTGACCCA GTCATCATCC ATTTTCGAGGT GTCCATGTCT 120
195
196 CAGCTGGTGA AGGTGGATGA AGTAAACCAG ATCATGGAGA CCAACCTGTG GCTCAAGCAA 180
197
198 ATCTGGAATG ACTACAAGCT GAAGTGGAAC CCCTCTGACT ATGGTGGGGC AGAGTTCATG 240
199
200 CGTGTCCCTG CACAGAAGAT CTGGAAGCCA GACATTGT 278
201 (2) INFORMATION FOR SEQ ID NO:6:
202
203 (i) SEQUENCE CHARACTERISTICS:
204 (A) LENGTH: 300 base pairs

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205 (B) TYPE: nucleic acid
206 (C) STRANDEDNESS: both
207 (D) TOPOLOGY: both
208
209 (ii) MOLECULE TYPE: cDNA
210
211
212 (ix) FEATURE:
213 (A) NAME/KEY: misc_feature
214 (B) LOCATION: 1..300
215 (D) OTHER INFORMATION: /note= "Rat neuronal NACHR alpha-3
216 cDNA shown as bottom sequence of Fig 8A."
217
218
219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
220
221 GATGCTGCTG CCAGCGGCCA GTGCCTCAGA AGCTGAGCAC CGCCTGTTCC AGTACCTGTT 60
222
223 CGAAGATTAC AACGAGATCA TCCGGCCAGT GGCTAATGTG TCCCATCCAG TCATCATCCA 120
224
225 GTTTGAGGTG TCCATGTCTC AGCTGGTGAA GGTGGATGAA GTAAACCAGA TCATGGAAAC 180
226
227 CAACCTGTGG CTGAAGCAAA TCTGGAATGA CTACAAGCTG AAATGGAAAC CCTCTGACTA 240
228
229 CCAAGGGGTG GAGTTCATGC GTGTTCTCCTGC AGAGAAGATC TGGAAACCAG ACATCGTACT 300
230
231
232 (2) INFORMATION FOR SEQ ID NO:7:
233
234 (i) SEQUENCE CHARACTERISTICS:
235 (A) LENGTH: 305 base pairs
236 (B) TYPE: nucleic acid
237 (C) STRANDEDNESS: both
238 (D) TOPOLOGY: both
239
240 (ii) MOLECULE TYPE: cDNA
241
242
243 (ix) FEATURE:
244 (A) NAME/KEY: misc_feature
245 (B) LOCATION: 1..305
246 (D) OTHER INFORMATION: /note= "Human neuronal NACHR
247 alpha-3 cDNA shown as top sequence in Fig 8B."
248
249
250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
251
252 TTCCAGGTGG ACGACAAGAC CAAAGCCTTA CTCAAGTACA CTGGGGACGT GACTTGGATA 60
253
254 CCTCCGGCCA TCTTTAAGAG CTCCTGTAAA ATCGACGTGA CCTACTTCCC GTTTGATTAC 120
255

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256 CAAAACTGTA CCATGAAGTT CGGTTCTCTGG TCCTACGATA AGGCGAAAAT CGATCTGGTC 180
257
258 CTGATCGGCT CTTCCATGAA CCTCAAGGAC TATTGGGAGA GCGGCGAGTG GGCCATCATC 240
259
260 AAAGCCCCAG GCTACAAACA CGACATCAAG TACAACTGCT GCGAGGAGAT CTACCCCCGAC 300
261
262 ATCAC 305
263
264
265
266
267

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..350
(D) OTHER INFORMATION: /note= "Rat neuronal NACHR alpha-3
cDNA shown as bottom sequence in Fig 8B."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

287
288 GTACAACAAC GCTGATGGGG ATTTCCAGGT GGATGACAAG ACCAAAGCTC TACTCAAGTA 60
289
290 CACAGGAGAA GTGACTTGGA TCCCGCCGGC CATCTTTAAG AGCTCATGCA AAATCGACGT 120
291
292 GACCTACTTC CCATTCGACT ACCAAAAGT CACCATGAAG TTCGGCTCCT GGTCTTACGA 180
293
294 CAAGGCAAAG ATCGACCTGG TCCTCATCGG CTCCTCCATG AACCTCAAGG ACTACTGGGA 240
295
296 GAGTGGCGAG TGGGCTATCA TTAAAGCCCC GGGCTACAAA CATGAAATCA AGTACAACTG 300
297
298 CTGTGAGGAG ATCTACCAAG ACATCACGTA CTCGCTGTAC ATCCGTCGCC 350
299

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

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307
308 (ii) MOLECULE TYPE: cDNA
309
310
311 (ix) FEATURE:
312 (A) NAME/KEY: misc_feature
313 (B) LOCATION: 1..1521
314 (D) OTHER INFORMATION: /note= "Human neuronal NACHR beta-2
315 cDNA shown as top sequence in Fig 9."
316
317
318 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
319
320 ATGCCCGCTG GCATGGCCCG GCGCTGCGGC CCCGTGGCGC TGCTCCTTGG CTTGGCCTC 60
321
322 CTCCGGCTGT GCTCAGGGGT GTGGGGTACG GATACAGAGG AGCGGCTGGT GGAGCATCTC 120
323
324 CTGGATCCTT CCCGCTACAA CAAGCTTATC CGCCCAGCCA CCAATGGCTC TGAGCTGGTG 180
325
326 ACAGTACAGC TTATGGTGTC ACTGGCCCAG CTCATCAGTG TGCATGAGCG GGAGCAGATC 240
327
328 ATGACCACCA ATGTCTGGCT GACCCAGGAG TGGGAAGATT ATCGCCTCAC CTGGAAGCCT 300
329
330 GAAGAGTTTG ACAACATGAA GAAAGTTCGG CTCCCTTCCA AACACATCTG GCTCCAGAT 360
331
332 GTGGTCCTGT ACAACAATGC TGACGGCATG TACGAGGTGT CTTTCTATTC CAATGCCGTG 420
333
334 GTCTCCTATG ATGGCAGCAT CTTCTGGCTG CCGCCTGCCA TCTACAAGAG CGCATGCAAG 480
335 ATTGAAGTAA AGCACTTCCC ATTTGACCAG CAGAACTGCA CCATGAAGTT CCGTTCGTGG 540
336
337 ACCTACGACC GCACAGAGAT CGACTTGGTG CTGAAGAGTG AGGTGGCCAG CCTGGACGAC 600
338
339 TTCACACCTA GTGGTGAGTG GGACATCGTG GCGCTGCCGG GCCGCGCAA CGAGAACCCC 660
340
341 GACGACTCTA CGTACGTGGA CATCACGTAT GACTTCATCA TTCGCCGCAA GCCGCTCTTC 720
342
343 TACACCATCA ACCTCATCAT CCCCTGTGTG CTCATCACCT CGCTAGCCAT CCTTGTCTTC 780
344
345 TACCTGCCAT CCGACTGTGG CGAGAAGATG ACGTTGTGCA TCTCAGTGCT GCTGGCGCTC 840
346
347 ACGGTCTTCC TGCTGCTCAT CTCCAAGATC GTGCCTCCCA CCTCCCTCGA CGTGCCGCTC 900
348
349 GTCGGCAAGT ACCTCATGTT CACCATGGTG CTTGTACCT TCTCCATCGT CACCAGCGTG 960
350
351 TGCGTGCTCA ACGTGACCA CCGCTCGCCC ACCACGCACA CCATGGCGCC CTGGGTGAAG 1020
352
353 GTCGTCTTCC TGGAGAAGCT GCCCGCGCTG CTCTTCATGC AGCAGCCACG CCATCATTGC 1080
354
355 GCCCGTCAGC GCCTGCGCCT GCGGCGACGC CAGCGTGAGC GCGAGGGCGC TGGAGCCCTC 1140
356
357 TTCTTCCGCG AAGCCCCAGG GGCCGACTCC TGCACGTGCT TCGTCAACCG CGCGTCGGTG 1200

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358
359 CAGGGGTTGG CCGGGGCCTT CGGGGCTGAG CCTGCACCAG TGGCGGGCCC CGGGCGCTCA      1260
360
361 GGGGAGCCGT GTGGCTGTGG CCTCCGGGAG GCGGTGGACG GCGTGCCTT CATCGCAGAC      1320
362
363 CACATGCGGA GCGAGGACGA TGACCAGAGC GTGAGTGAGG ACTGGAAGTA CGTCGCCATG      1380
364
365 GTGATCGACC GCCTCTTCCT CTGGATCTTT GTCTTTGTCT GTGTCTTTGG CACCATCGGC      1440
366
367 ATGTTCTTGC AGCCTCTCTT CCAGAACTAC ACCACCACCA CCTTCCTCCA CTCAGACCAC      1500
368
369 TCAGCCCCCA GCTCCAAGTG A                                          1521
370
371 (2) INFORMATION FOR SEQ ID NO:10:
372
373     (i) SEQUENCE CHARACTERISTICS:
374         (A) LENGTH: 1512 base pairs
375         (B) TYPE: nucleic acid
376         (C) STRANDEDNESS: both
377         (D) TOPOLOGY: both
378
379     (ii) MOLECULE TYPE: cDNA
380
381
382     (ix) FEATURE:
383         (A) NAME/KEY: misc_feature
384         (B) LOCATION: 1..1512
385         (D) OTHER INFORMATION: /note= "Rat neuronal NACHR beta-2
386             cDNA shown as bottom nucleotide sequence in Figure
387             9."
388
389
390     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
391
392 ATGCTGGCTT GCATGGCCGG GCACTCCAAC TCAATGGCGC TGTTAGCTT CAGCCTTCTT      60
393
394 TGGCTGTGCT CAGGGGTTTT GGGAACTGAC ACAGAGGAGC GGCTAGTGGA GCATCTCTTA      120
395
396 GATCCCTCCC GCTATAACAA GCTGATTCGT CCAGCTACTA ACGGCTCTGA GCTGGTGACT      180
397
398 GTACAGCTCA TGGTATCATT GGCTCAGCTC ATTAGTGTGC ACGAGCGGGA GCAGATCATG      240
399
400 ACCACCAATG TCTGGCTGAC CCAGGAGTGG GAAGATTACC GCCTCACATG GAAGCCTGAG      300
401
402 GACTTCGACA ATATGAAGAA AGTCCGGCTC CCTTCCAAAC ACATCTGGCT CCCAGATGTG      360
403
404 GTTCTATACA ACAATGCTGA CGGCATGTAC GAAGTCTCCT TCTATTCCAA TGCTGTGGTC      420
405
406 TCCTATGATG GCAGCATCTT TTGGCTACCA CCTGCCATCT ACAAGAGTGC ATGCAAGATT      480
407
408 GAGGTGAAGC ACTTCCCATT TGACCAGCAG AATTGCACCA TGAAGTTTCG CTCATGGACC      540
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409
410 TACGACCGTA CTGAGATTGA CCTGGTGCTC AAAAGTGATG TGGCCAGTCT GGATGACTTC 600
411
412 ACACCCAGCG GGGAGTGGGA CATCATCGCA CTGCCAGGCC GACGCAACGA GAACCCAGAC 660
413
414 GACTCCACCT ATGTGGACAT CACCTATGAC TTCATCATTC GTCGCAAACC ACTCTTCTAC 720
415
416 ACTATCAACC TCATCATCCC CTGCGTACTC ATCACCTCGC TGGCCATCCT GGTCTTCTAC 780
417
418 CTGCCCTCAG ACTGTGGTGA AAAGATGACA CTTTGTATTT CTGTGCTGCT AGCACTCACG 840
419
420 GTGTTCCCTGC TGCTCATCTC CAAGATTGTG CCTCCACCT CCCTCGATGT ACCGCTGGTG 900
421
422 GGCAAGTACC TCATGTTTAC CATGGTGCTA GTCACCTTCT CCATCGTCAC CAGCGTGTGT 960
423
424 GTGCTCAATG TGCACCACCG CTCGCCTACC ACGCACACCA TGGCCCCCTG GGTCAAGGTG 1020
425
426 GTCTTCCTGG AGAAGCTGCC CACCCTGCTC TTCCTGCAGC AGCCACGCCA CCGCTGTGCA 1080
427
428 CGTCAGCGTC TGCGCTTGAG GAGGCGCCAG CGAGAGCGTG AGGGCGAGGC GGTTCCTTCTC 1140
429
430 CGTGAAGGTC CTGCGGCTGA CCCATGTACC TGCTTTGTCA ACCCTGCATC AGTGCAGGGC 1200
431
432 TTGGCTGGGG CTTTCCGAGC TGAGCCCACT GCAGCCGGCC CGGGGCGCTC TGTGGGGCCA 1260
433
434 TGCAGCTGTG GCCTCCGGA AGCAGTGGAT GCGGTACGCT TCATTGCGGA CCACATGCGA 1320
435
436 AGTGAGGATG ATGACCAGAG TGTGAGGGAG GACTGGAAAT ACGTTGCCAT GGTGATCGAC 1380
437
438 CGCCTGTTCC TGTGGATCTT TGTCTTTGTC TGTGTCTTTG GGACCGTCGG CATGTTCTCTG 1440
439
440 CAGCCTCTCT TCCAGAACTA CACTGCCACT ACCTTCCTCC ACCCTGACCA CTCAGCTCCC 1500
441
442 AGCTCCAAGT GA 1512

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCTTTCGAT ATCAGAATTC G

21

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460
461 (2) INFORMATION FOR SEQ ID NO:12:
462
463 (i) SEQUENCE CHARACTERISTICS:
464 (A) LENGTH: 21 base pairs
465 (B) TYPE: nucleic acid
466 (C) STRANDEDNESS: single
467 (D) TOPOLOGY: linear
468
469 (ii) MOLECULE TYPE: DNA (genomic)
470
471
472 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
473
474 AGCTCGAATT CTGATATCGA A
475

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SEQUENCE VERIFICATION REPORT
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SEQUENCE CORRECTION REPORT
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